

SEQUENCE LISTING

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<120> Compositions and Methods for the Detection, Diagnosis
 and Therapy of Hematological Malignancies

<130> 014058-014402PC

<140> WO PCT/US03/02353

<141> 2003-01-22

<150> US 10/057,475

<151> 2002-01-22

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<170> PatentIn Ver. 2.1

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Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu Val Thr Ile Gln
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Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn Arg Asn Arg Glu Arg
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Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys
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Lys Asn Asp Ser Gly Ile Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu
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Gln Gln Pro Ser Thr Gln Glu Tyr Val Leu His Val Tyr Glu His Leu
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Ser Lys Pro Lys Val Thr Met Gly Leu Gln Ser Asn Lys Asn Gly Thr
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 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
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Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
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Thr Asn Phe Ile Lys Ala Glu Tyr Lys Gly Arg Val Thr Leu Lys Gln
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Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu
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Ser Asp Ser Gly Val Tyr Ala Cys Gly Ala Gly Met Asn Thr Asp Arg
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Gly Lys Thr Gln Lys Val Thr Leu Asn Val His Ser Glu Tyr Glu Pro
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Ser Trp Glu Glu Gln Pro Met Pro Glu Thr Pro Lys Trp Phe His Leu
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Pro Tyr Leu Phe Gln Met Pro Ala Tyr Ala Ser Ser Ser Lys Phe Val
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Thr Arg Val Thr Thr Pro Ala Gln Arg Gly Lys Val Pro Pro Val His
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His Ser Ser Pro Thr Thr Gln Ile Thr His Arg Pro Arg Val Ser Arg
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Ala Ser Ser Val Ala Gly Asp Lys Pro Arg Thr Phe Leu Pro Ser Thr
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Thr Ala Ser Lys Ile Ser Ala Leu Glu Gly Leu Leu Lys Pro Gln Thr
210 215 220

Pro Ser Tyr Asn His His Thr Arg Leu His Arg Gln Arg Ala Leu Asp
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Tyr Gly Ser Gln Ser Gly Arg Glu Gly Gln Gly Phe His Ile Leu Ile
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Pro Thr Ile Leu Gly Leu Phe Leu Leu Ala Leu Leu Gly Leu Val Val
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Lys Arg Ala Val Glu Arg Arg Lys Ala Leu Ser Arg Arg Ala Arg Arg
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 Arg Ala Arg Gly Ala Asp Ala Ala Gly Thr Gly Glu Ala Pro Val Pro
 325 330 335
 Gly Pro Gly Ala Pro Leu Pro Pro Ala Pro Leu Gln Val Ser Glu Ser
 340 345 350
 Pro Trp Leu His Ala Pro Ser Leu Lys Thr Ser Cys Glu Tyr Val Ser
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reading frame His tag fusion

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      35              40              45

Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln
      50              55              60

Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala
      65              70              75              80

Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly
      85              90              95

Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser
      100              105              110

Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser
      115              120              125

Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val
      130              135              140

Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile
      145              150              155              160

Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro
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Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg
      180              185              190

Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro
      195              200              205

Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile
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Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln Gln
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 Tyr Phe Cys Asp Cys Cys His Ser Tyr Ala Glu Ser Cys Ile Pro Ala
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<211> 662

<212> PRT

<213> Homo sapiens

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Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
 35             40             45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
 50             55             60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
 65             70             75             80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
 85             90             95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
100             105             110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
115             120             125

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 Lys Cys Asn Ile Leu Ser Gln Gln Gln Thr Glu Ser Trp Ser Lys Glu
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 Asp Thr Asn Ile Lys Gln Glu Ser Gly Ser Ser Thr Ser Ser Tyr Ser
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<210> 12
 <211> 635
 <212> PRT
 <213> Homo sapiens

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  20              25              30

Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
  35              40              45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
  50              55              60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
  65              70              75              80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
  85              90              95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
  100             105             110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
  115             120             125

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Leu	Ser	Ser	Thr	Glu	Val	His	Met	Val	Arg	Pro	Gly	Tyr	Ser	His	Arg	130	135	140
Val	Ser	Leu	Pro	Thr	Ser	Pro	Gly	Ile	Leu	Ala	Thr	Ser	Pro	Tyr	Pro	145	150	155
Glu	Thr	Asp	Ser	Ala	Phe	Phe	Glu	Pro	Ser	His	Leu	Thr	Ser	Ala	Ala	165	170	175
Asp	Glu	Gly	Ala	Val	Gln	Val	Ser	Arg	Arg	Thr	Ile	Ser	Ser	Asn	Ser	180	185	190
Phe	Ser	Pro	Glu	Val	Phe	Val	Leu	Pro	Val	Asp	Val	Glu	Lys	Glu	Asn	195	200	205
Ala	His	Phe	Tyr	Val	Ala	Asp	Met	Ile	Ile	Ser	Ala	Met	Glu	Lys	Met	210	215	220
Lys	Cys	Asn	Ile	Leu	Ser	Gln	Gln	Gln	Thr	Glu	Ser	Trp	Ser	Lys	Glu	225	230	235
Val	Ser	Gly	Leu	Leu	Gly	Ser	Asp	Gln	Pro	Asp	Ser	Glu	Met	Thr	Phe	245	250	255
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 <213> Homo sapiens

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<211> 1033

<212> PRT

<213> Homo sapiens

<400> 15

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Arg	Ile	Ser	Tyr	Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg
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Cys	Ile	Thr	Lys	Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro
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Pro	Gly	Gly	Tyr	Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp
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Ser	Val	Thr	Phe	Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys
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Ser	Val	Trp	Cys	Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro
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Thr	Cys	Val	Ser	Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile
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His	Asn	Gly	His	His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly
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Leu	Ser	Val	Thr	Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu
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Lys	Ile	Ile	Asn	Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro
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Phe	Cys	Asp	Glu	Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys
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Val	Ile	Ala	Gly	Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Glu
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 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
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 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
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 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
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 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
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 465 470 475 480
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
 485 490 495
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
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 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
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 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
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 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
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 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
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 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
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 625 630 635 640
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 645 650 655
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
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 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
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 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
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 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
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 820 825 830
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
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 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
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 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
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Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
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Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
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Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
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Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
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Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
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Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
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<400> 18

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Ala	Val	Gly	Gln	Leu	Gly	Val	Arg	Val	Phe	His	Ser	Ser	Pro	Ala	Ala	35	40	45	
Ser	Ser	Leu	Asp	Phe	Ile	Gly	Gly	Pro	Ala	Ile	Leu	Leu	Gly	Leu	Ile	50	55	60	
Ser	Leu	Ala	Thr	Asp	Asp	His	Thr	Met	Tyr	Ala	Ala	Val	Lys	Val	Leu	65	70	75	80
His	Ser	Val	Leu	Thr	Ser	Asn	Ala	Met	Cys	Asp	Phe	Leu	Met	Gln	His	85	90	95	
Ile	Cys	Gly	Tyr	Gln	Ile	Met	Ala	Phe	Leu	Leu	Arg	Lys	Lys	Ala	Ser	100	105	110	
Leu	Leu	Asn	His	Arg	Ile	Phe	Gln	Leu	Ile	Leu	Ser	Val	Ala	Gly	Thr	115	120	125	
Val	Glu	Leu	Gly	Phe	Arg	Ser	Ser	Ala	Ile	Thr	Asn	Thr	Gly	Val	Phe	130	135	140	
Gln	His	Ile	Leu	Cys	Asn	Phe	Glu	Leu	Trp	Met	Asn	Thr	Ala	Asp	Asn	145	150	155	160
Leu	Glu	Leu	Ser	Leu	Phe	Ser	His	Leu	Leu	Glu	Ile	Leu	Gln	Ser	Pro	165	170	175	
Arg	Glu	Gly	Pro	Arg	Asn	Ala	Glu	Ala	Ala	His	Gln	Ala	Gln	Leu	Ile	180	185	190	
Pro	Lys	Leu	Ile	Phe	Leu	Phe	Asn	Glu	Pro	Ser	Leu	Ile	Pro	Ser	Lys	195	200	205	
Ile	Pro	Thr	Ile	Ile	Gly	Ile	Leu	Ala	Cys	Gln	Leu	Arg	Gly	His	Phe	210	215	220	
Ser	Thr	Gln	Asp	Leu	Leu	Arg	Ile	Gly	Leu	Phe	Val	Val	Tyr	Thr	Leu	225	230	235	240
Lys	Pro	Ser	Ser	Val	Asn	Glu	Arg	Gln	Ile	Cys	Met	Asp	Gly	Ala	Leu	245	250	255	
Asp	Pro	Ser	Leu	Pro	Ala	Gly	Ser	Gln	Thr	Ser	Gly	Lys	Thr	Ile	Trp	260	265	270	

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 Gly Pro Asp Trp Phe Leu Leu Leu Leu Gln Gly His Leu His Ala Ser
 305 310 315 320
 Thr Thr Val Leu Ala Leu Lys Leu Leu Leu Tyr Phe Leu Ala Ser Pro
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 Ser Leu Arg Thr Arg Phe Arg Asp Gly Leu Cys Ala Gly Ser Trp Val
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 Glu Arg Ser Thr Glu Gly Val Asp Ile Val Met Asp Asn Leu Lys Ser
 355 360 365
 Gln Ser Pro Leu Pro Glu Gln Ser Pro Cys Leu Leu Pro Gly Phe Arg
 370 375 380
 Val Leu Asn Asp Phe Leu Ala His His Val His Ile Pro Glu Val Tyr
 385 390 395 400
 Leu Ile Val Ser Thr Phe Phe Leu Gln Thr Pro Leu Thr Glu Leu Met
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 Asp Gly Pro Lys Asp Ser Leu Asp Ala Met Leu Gln Trp Leu Leu Gln
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 Arg His His Gln Glu Glu Val Leu Gln Ala Gly Leu Cys Thr Glu Gly
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 Ser Pro Glu Ala Ala Ala Glu Gly Asp Ser Thr Val Glu Gly Leu Gln
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 Gln Leu Leu Leu Arg Glu Leu Leu Leu Gly Ala Ser Ser Pro Lys Gln
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 Trp Leu Pro Leu Glu Val Leu Leu Glu Ala Ser Pro Asp His Ala Thr
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 Gly Lys Glu Pro Gln Pro Ser Ala Glu Ala Ala Ala Pro Ser Leu
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 Gln Thr Leu Glu Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly
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 Glu Arg Glu Val Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr
 835 840 845
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 865 870 875 880
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 Asp Pro Glu Cys Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr
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Arg Arg Arg Gly Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val
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 930 935 940
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 Ser Ser Gly Arg His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser
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 Gly Glu Pro Asp Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe
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 Pro Ala Leu His Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys
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 Arg Glu Arg Gln Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val
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 Thr Gln Lys Phe Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu
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 Gly Val Leu Leu Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe
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 Thr Leu Ser Pro Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser
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Glu Ser Pro Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr
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Ile Leu Ala Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn
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<211> 321

<212> PRT

<213> Homo sapiens

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Ser Gln Val Ser Lys Asn Leu Glu Ser His His Gly Asp Gln Met Ala
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Gln Lys Ser Gln Ser Thr Gln Ile Ser Gln Glu Leu Glu Glu Leu Arg
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Ala Glu Gln Gln Arg Leu Lys Ser Gln Asp Leu Glu Leu Ser Trp Asn
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Leu Asn Gly Leu Gln Ala Asp Leu Ser Ser Phe Lys Ser Gln Glu Leu
115 120 125

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Val Thr Lys Leu Arg Met Glu Leu Gln Val Ser Ser Gly Phe Val Cys
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165 170 175

Phe Gly Lys Gly Thr Lys Gln Trp Val His Ala Arg Tyr Ala Cys Asp
180 185 190

Asp Met Glu Gly Gln Leu Val Ser Ile His Ser Pro Glu Glu Gln Asp
195 200 205

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210 215 220

Asn Leu Asp Leu Lys Gly Glu Phe Ile Trp Val Asp Gly Ser His Val
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Asp Tyr Ser Asn Trp Ala Pro Gly Glu Pro Thr Ser Arg Ser Gln Gly
245 250 255

Glu Asp Cys Val Met Met Arg Gly Ser Gly Arg Trp Asn Asp Ala Phe
260 265 270

Cys Asp Arg Lys Leu Gly Ala Trp Val Cys Asp Arg Leu Ala Thr Cys
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<212> PRT

<213> Homo sapiens

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Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
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Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly
115 120 125
Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
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Phe Gln Cys Asn Gln Cys Ser Ser Ala Leu Ser Gly Val Gly Gly Ile
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Cys His Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Met Tyr Pro Val
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<212> PRT

<213> Homo sapiens

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Val Cys Gly Met Val Ala Ala Leu Ser Ala Ile Arg Ala Asn Cys His
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Gln Glu Pro Ser Val Cys Leu Gln Ala Ala Cys Pro Glu Ser Trp Ile
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Gly Phe Gln Arg Lys Cys Phe Tyr Phe Ser Asp Asp Thr Lys Asn Trp
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Thr Ser Ser Gln Arg Phe Cys Asp Ser Gln Asp Ala Asp Leu Ala Gln
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Val Glu Ser Phe Gln Glu Leu Asn Phe Leu Leu Arg Tyr Lys Gly Pro
 115              120              125

Ser Asp His Trp Ile Gly Leu Ser Arg Glu Gln Gly Gln Pro Trp Lys
 130              135              140

Trp Ile Asn Gly Thr Glu Trp Thr Arg Gln Phe Pro Ile Leu Gly Ala
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 Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe
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Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr
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ataaaaagatt tgggtgctaca aaagaagcag ctgaaaaaac aagaacagtt tttagtact 1920
atttacatcc acagtataag gcacctacag aaaaccattc aaggccctac tatgcaaaaa 1980
gatggaagga agaaaagcca gttcacttta aagaattcag aaaaaataca aattcaaaga 2040
aatgcagtc tgggcatgat tgtagagaaa attctcattc tttcagaaag gcttgttctg 2100
gtgtatttga ttgtgctcaa caagagtcca tgagcctttt taacacagtg gtgatcccta 2160
taaggatgga tgaatttaga cagataattc aaaggtacat gttaaaagaa ctggatactt 2220
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tacatgatca gaagctcttc actgactttg ttaatgatgt taagattatc ttaggaaaca 2340
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aacgtgatca ctttgacttg agcaaattgg ttaattttta tcttaaaatc agttaagaat 2700
atataaaatc ctaccttttg ccaagtttgt ttcttttcat tatagtttat atgaaaagat 2760
caccttaagt gaaattattt tccttatttt cctttaatct tttatgtatt tattcacttc 2820
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attatctttg ataaaggtag aggcacaaaag aggcaaaacta acaagtcaaa ttctaattgtg 3000
tgtacttcat aataattttt tatccatttt catcttcttt atctttatat tctgtaacat 3060
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<210> 35

<211> 755

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Glu Asn Ser Ser Asp Ser Asp Ser Ser Cys Gly Trp Thr Val
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Ile Ser His Glu Gly Ser Asp Ile Glu Met Leu Asn Ser Val Thr Pro
20 25 30

Thr Asp Ser Cys Glu Pro Ala Pro Glu Cys Ser Ser Leu Glu Gln Glu
35 40 45

Glu Leu Gln Ala Leu Gln Ile Glu Gln Gly Glu Ser Ser Gln Asn Gly
50 55 60

Thr	Val	Leu	Met	Glu	Glu	Thr	Ala	Tyr	Pro	Ala	Leu	Glu	Glu	Thr	Ser	65	70	75	80
Ser	Thr	Ile	Glu	Ala	Glu	Glu	Gln	Lys	Ile	Pro	Glu	Asp	Ser	Ile	Tyr	85	90	95	
Ile	Gly	Thr	Ala	Ser	Asp	Asp	Ser	Asp	Ile	Val	Thr	Leu	Glu	Pro	Pro	100	105	110	
Lys	Leu	Glu	Glu	Ile	Gly	Asn	Gln	Glu	Val	Val	Ile	Val	Glu	Glu	Ala	115	120	125	
Gln	Ser	Ser	Glu	Asp	Phe	Asn	Met	Gly	Ser	Ser	Ser	Ser	Ser	Gln	Tyr	130	135	140	
Thr	Phe	Cys	Gln	Pro	Glu	Thr	Val	Phe	Ser	Ser	Gln	Pro	Ser	Asp	Asp	145	150	155	160
Glu	Ser	Ser	Ser	Asp	Glu	Thr	Ser	Asn	Gln	Pro	Ser	Pro	Ala	Phe	Arg	165	170	175	
Arg	Arg	Arg	Ala	Arg	Lys	Lys	Thr	Val	Ser	Ala	Ser	Glu	Ser	Glu	Asp	180	185	190	
Arg	Leu	Val	Ala	Glu	Gln	Glu	Thr	Glu	Pro	Ser	Lys	Glu	Leu	Ser	Lys	195	200	205	
Arg	Gln	Phe	Ser	Ser	Gly	Leu	Asn	Lys	Cys	Val	Ile	Leu	Ala	Leu	Val	210	215	220	
Ile	Ala	Ile	Ser	Met	Gly	Phe	Gly	His	Phe	Tyr	Gly	Thr	Ile	Gln	Ile	225	230	235	240
Gln	Lys	Arg	Gln	Gln	Leu	Val	Arg	Lys	Ile	His	Glu	Asp	Glu	Leu	Asn	245	250	255	
Asp	Met	Lys	Asp	Tyr	Leu	Ser	Gln	Cys	Gln	Gln	Glu	Gln	Glu	Ser	Phe	260	265	270	
Ile	Asp	Tyr	Lys	Ser	Leu	Lys	Glu	Asn	Leu	Ala	Arg	Cys	Trp	Thr	Leu	275	280	285	
Thr	Glu	Ala	Glu	Lys	Met	Ser	Phe	Glu	Thr	Gln	Lys	Thr	Asn	Leu	Ala	290	295	300	
Thr	Glu	Asn	Gln	Tyr	Leu	Arg	Val	Ser	Leu	Glu	Lys	Glu	Glu	Lys	Ala	305	310	315	320
Leu	Ser	Ser	Leu	Gln	Glu	Glu	Leu	Asn	Lys	Leu	Arg	Glu	Gln	Ile	Arg	325	330	335	
Ile	Leu	Glu	Asp	Lys	Gly	Thr	Ser	Thr	Glu	Leu	Val	Lys	Glu	Asn	Gln	340	345	350	
Lys	Leu	Lys	Gln	His	Leu	Glu	Glu	Glu	Lys	Gln	Lys	Lys	His	Ser	Phe	355	360	365	
Leu	Ser	Gln	Arg	Glu	Thr	Leu	Leu	Thr	Glu	Ala	Lys	Met	Leu	Lys	Arg	370	375	380	

Glu Leu Glu Arg Glu Arg Leu Val Thr Thr Ala Leu Arg Gly Glu Leu
 385 390 395 400
 Gln Gln Leu Ser Gly Ser Gln Leu His Gly Lys Ser Asp Ser Pro Asn
 405 410 415
 Val Tyr Thr Glu Lys Lys Glu Ile Ala Ile Leu Arg Glu Arg Leu Thr
 420 425 430
 Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg Ser Asp Leu Trp
 435 440 445
 Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly Lys Gln Gly Thr
 450 455 460
 Asp Gly Lys Lys Lys Gly Gly Arg Gly Ser His Arg Ala Lys Asn Lys
 465 470 475 480
 Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr Phe Asp Ala Met
 485 490 495
 Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys Glu Lys Ile Lys
 500 505 510
 Gln Ala Lys Glu Ala Val Lys Glu Asn Leu Lys Lys Phe Ser Asp Ser
 515 520 525
 Val Lys Ser Thr Phe Arg His Phe Lys Asp Thr Thr Lys Asn Ile Phe
 530 535 540
 Asp Glu Lys Gly Asn Lys Arg Phe Gly Ala Thr Lys Glu Ala Ala Glu
 545 550 555 560
 Lys Pro Arg Thr Val Phe Ser Asp Tyr Leu His Pro Gln Tyr Lys Ala
 565 570 575
 Pro Thr Glu Asn His Ser Arg Pro Tyr Tyr Ala Lys Arg Trp Lys Glu
 580 585 590
 Glu Lys Pro Val His Phe Lys Glu Phe Arg Lys Asn Thr Asn Ser Lys
 595 600 605
 Lys Cys Ser Pro Gly His Asp Cys Arg Glu Asn Ser His Ser Phe Arg
 610 615 620
 Lys Ala Cys Ser Gly Val Phe Asp Cys Ala Gln Gln Glu Ser Met Ser
 625 630 635 640
 Leu Phe Asn Thr Val Val Ile Pro Ile Arg Met Asp Glu Phe Arg Gln
 645 650 655
 Ile Ile Gln Arg Tyr Met Leu Lys Glu Leu Asp Thr Phe Cys Arg Trp
 660 665 670
 Asn Glu Leu Asp Gln Phe Ile Asn Lys Phe Phe Leu Asn Gly Val Phe
 675 680 685
 Ile His Asp Gln Lys Leu Phe Thr Asp Phe Val Asn Asp Val Lys Ile
 690 695 700

Ile Leu Gly Asn Met Lys Glu Tyr Glu Val Asp Asn Asp Gly Val Phe
 705 710 715 720

Glu Lys Leu Asp Glu Tyr Ile Tyr Arg His Phe Phe Gly His Thr Phe
 725 730 735

Ser Pro Pro Tyr Gly Pro Arg Ser Val Tyr Ile Lys Pro Cys His Tyr
 740 745 750

Ser Ser Leu
 755

<210> 36
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1)..(558)
 <223> n = g, a, c or t

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 tgggtgtttgc atccaggggt ccagcaggat ctcttccagt gagggtcggg aagaaggttt 180
 gggggccagg caccggcggg ttagggcaca gcaatcttgg ggaaaacatg ggcttgggaa 240
 gtggagctca gcttccagaa tctcctgggc cctctcaaag ggaatgtccc cacacaccat 300
 gtcataagagg aggatgccca gtgaccagac agtggccggg agtgcattgt actggtgtcg 360
 agagatccac tctggggggc tgtacaccct tgtcccatca aagtcagtgt agggttcatc 420
 atgaagcagg gcaccagaac caaaatcaat gagtttggca cagccacggc gtaggtctat 480
 caggatgntc tcatccttga tgtcacgatg gacaactnca cgggaaatgg cagtgtctga 540
 tggctgccac tactttgg 558

<210> 37
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (1)..(86)
 <223> Xaa = any amino acid

<400> 37
 Gln Val Val Ala Xaa Ile Gln His Cys His Ser Arg Gly Val Val His
 1 5 10 15
 Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly Cys
 20 25 30
 Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro
 35 40 45
 Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile
 50 55 60

Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly
65 70 75 80

Ile Xaa Leu Tyr Asp Met
85

<210> 38

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(584)

<223> n = g, a, c or t

<400> 38

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tgattattta	catttttagta	attggacaat	ccgggctcag	gaggaggttg	caagaatctg	120
caaaagttgg	agggagcgcc	ccaggagaac	aaacagcaag	ccttatttcc	cctagcccat	180
ccccaaaaa	accatccatc	ccatcctagt	gtctgggtgg	gtccggtggg	gtccatcttc	240
cattccttcc	caaattatgg	aagtaaggtt	cttctcacca	gaataagagc	acttgggata	300
acagagtagg	gtcccctcac	ccaaaaaaaa	aaaaaaaaan	gaagccttgg	ggtaacaaca	360
gggcattacc	tccccagaa	taaagaatcc	tgggctgagg	caggtaagca	gcttgacca	420
atatgggacc	ctaggctagg	ggaaagggtc	cctttactaa	aataaaagct	actgggggat	480
tggaaggaaa	gcacccttgc	ccaagtaaga	gcatatgaac	taagtttgng	tggnggtagt	540
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<210> 39

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 39

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tgctttccac	cctggcgccc	cccagccctg	gctccccage	tgcgctgccc	cgggcggtcca	120
cgccctgcgg	gcttagcggg	ttcagtgggc	tcaatctgcg	cagcgccacc	tccatgttga	180
ccaagcctct	acaggggcct	cccgcgcccc	ccgggacccc	cacgcccgcg	ccaggaggca	240
aggatcggga	agcggttcgag	gccgagtatc	gactcggccc	cctcctgggt	aagggggggt	300
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ttccccgaa	tcgtgtgctg	ggctgggtccc	ccttgtcaga	ctcagtcaca	tgcccactcg	420
aagtgcact	gctatggaaa	gtgggtgcag	gtgggtggga	ccctggcggt	atccgcctgc	480
ttgactgggt	tgagacacag	gagggcttca	tgctggctct	cgagcgccct	ttgcccgcgc	540
aggatctctt	tgactatata	acagagaagg	gccactggg	tgaaggccca	agccgctgct	600
tccttgccca	agtagtggca	gccatccagc	actgccattc	ccgtggagtt	gtccatcggt	660
acatcaagga	tgagaacatc	ctgatagacc	tacgccgtgg	ctgtgccaaa	ctcattgatt	720
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cccctttggc	ctggctcctg	ctaccctaag	cctggcctgg	cctggcctgg	cccccaatgg	1140
tcagaagagc	catcccattg	ccatgtcaca	gggatagatg	gacatttggt	gacttggttt	1200
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ggtagaaga	cataaaccaa	gtctgccag	ttcccttccc	aatcctacaa	aggagccttc	1320
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ggaagtttat	tttgggtgaag	ttgttcccat	tctgagcccc	gggactctta	ttctgatgat	1440
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cttgggcaag ggtgctttcc ttccaatacc ccagtagctt ttatttttagt aaagggaccc 1560
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aattactaaa atgtaaataa tcacgtattg tggggagggg agttccaagt gtgccctcct 1980
ctcttctcct gcctggatta tttaaaaagc catgtgtgga aaccactat ttaataaaaag 2040
taatagaatc ag 2052

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<210> 40
 <211> 311
 <212> PRT
 <213> Homo sapiens

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<400> 40
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Thr Pro Pro Pro Gly Gly Lys Asp Arg Glu Ala Phe Glu Ala Glu Tyr
      20              25              30

Arg Leu Gly Pro Leu Leu Gly Lys Gly Gly Phe Gly Thr Val Phe Ala
      35              40              45

Gly His Arg Leu Thr Asp Arg Leu Gln Val Ala Ile Lys Val Ile Pro
      50              55              60

Arg Asn Arg Val Leu Gly Trp Ser Pro Leu Ser Asp Ser Val Thr Cys
      65              70              75              80

Pro Leu Glu Val Ala Leu Leu Trp Lys Val Gly Ala Gly Gly Gly His
      85              90              95

Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe
      100             105             110

Met Leu Val Leu Glu Arg Pro Leu Pro Ala Gln Asp Leu Phe Asp Tyr
      115             120             125

Ile Thr Glu Lys Gly Pro Leu Gly Glu Gly Pro Ser Arg Cys Phe Phe
      130             135             140

Gly Gln Val Val Ala Ala Ile Gln His Cys His Ser Arg Gly Val Val
      145             150             155             160

His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly
      165             170             175

Cys Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu
      180             185             190

Pro Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp
      195             200             205

Ile Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu
      210             215             220

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Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg
 225 230 235 240
 Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser
 245 250 255
 Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser
 260 265 270
 Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr
 275 280 285
 Pro Ala Glu Asp Val Pro Leu Asn Pro Ser Lys Gly Gly Pro Ala Pro
 290 295 300
 Leu Ala Trp Ser Leu Leu Pro
 305 310

<210> 41
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1)..(105)
 <223> n = g, a, c or t

<400> 41
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 cttttggatg gttttctcta cnactcctc caagcttccn tccag 105

<210> 42
 <211> 1125
 <212> DNA
 <213> Homo sapiens

<400> 42
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 ctcttcttct tgcctctcgg cagcctgatc ttctgcttcg gcatctggat cctcatcgac 180
 aagaccagct tgcgtgcctt tgtgggcttg gccttcgtgc ctctgcagat ctggtccaaa 240
 gtccctggcca tctcaggaat cttcaccatg ggcacgcgcc tcctgggttg tgtggggggc 300
 ctcaaggagc tccgctgcct cctgggcctg tattttggga tgctgctgct cctggttgcc 360
 acacagatca cctgggaat cctcatctcc actcagcggg ccagctgga gcgaagcttg 420
 cgggacgtcg tagagaaaac catccaaaag tacggcacca acccgagga gaccgcggc 480
 gaggagagct gggactatgt gcagttccag ctgcgctgct gcggctggca ctaccgcag 540
 gactgggttc aagtcctcat cctgagaggt aacgggctcg aggcgcaccg cgtgccctgc 600
 tctgtctaca acttgctcggc gaccaacgac tccacaatcc tagataaggt gatcttgccc 660
 cagctcagca ggcttgga cctggcgcgg tccagacaca gtgcagacat ctgcgctgct 720
 cctgcagaga gccacatcta ccgcgagggc tgcgcgcagg gcctccagaa gtggctgcac 780
 aacaacctta tttccatagt gggcatttgc ctgggcgtcg gcctactcga gctcgggttc 840
 atgacgctct cgatattcct gtgcagaaac ctggaccacg tctacaaccg gctcgtcga 900
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<210> 43
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 43

Met	Ser	Ala	Gln	Glu	Ser	Cys	Leu	Ser	Leu	Ile	Lys	Tyr	Phe	Leu	Phe
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Val	Phe	Asn	Leu	Phe	Phe	Phe	Val	Leu	Gly	Ser	Leu	Ile	Phe	Cys	Phe
		20						25					30		
Gly	Ile	Trp	Ile	Leu	Ile	Asp	Lys	Thr	Ser	Phe	Val	Ser	Phe	Val	Gly
	35						40					45			
Leu	Ala	Phe	Val	Pro	Leu	Gln	Ile	Trp	Ser	Lys	Val	Leu	Ala	Ile	Ser
	50					55					60				
Gly	Ile	Phe	Thr	Met	Gly	Ile	Ala	Leu	Leu	Gly	Cys	Val	Gly	Ala	Leu
	65				70					75					80
Lys	Glu	Leu	Arg	Cys	Leu	Leu	Gly	Leu	Tyr	Phe	Gly	Met	Leu	Leu	Leu
				85					90					95	
Leu	Phe	Ala	Thr	Gln	Ile	Thr	Leu	Gly	Ile	Leu	Ile	Ser	Thr	Gln	Arg
		100						105					110		
Ala	Gln	Leu	Glu	Arg	Ser	Leu	Arg	Asp	Val	Val	Glu	Lys	Thr	Ile	Gln
		115					120					125			
Lys	Tyr	Gly	Thr	Asn	Pro	Glu	Glu	Thr	Ala	Ala	Glu	Glu	Ser	Trp	Asp
	130					135					140				
Tyr	Val	Gln	Phe	Gln	Leu	Arg	Cys	Cys	Gly	Trp	His	Tyr	Pro	Gln	Asp
	145				150				155						160
Trp	Phe	Gln	Val	Leu	Ile	Leu	Arg	Gly	Asn	Gly	Ser	Glu	Ala	His	Arg
			165						170					175	
Val	Pro	Cys	Ser	Cys	Tyr	Asn	Leu	Ser	Ala	Thr	Asn	Asp	Ser	Thr	Ile
		180						185					190		
Leu	Asp	Lys	Val	Ile	Leu	Pro	Gln	Leu	Ser	Arg	Leu	Gly	His	Leu	Ala
		195				200					205				
Arg	Ser	Arg	His	Ser	Ala	Asp	Ile	Cys	Ala	Val	Pro	Ala	Glu	Ser	His
	210					215					220				
Ile	Tyr	Arg	Glu	Gly	Cys	Ala	Gln	Gly	Leu	Gln	Lys	Trp	Leu	His	Asn
	225				230				235						240
Asn	Leu	Ile	Ser	Ile	Val	Gly	Ile	Cys	Leu	Gly	Val	Gly	Leu	Leu	Glu
			245						250				255		
Leu	Gly	Phe	Met	Thr	Leu	Ser	Ile	Phe	Leu	Cys	Arg	Asn	Leu	Asp	His
		260						265					270		
Val	Tyr	Asn	Arg	Leu	Ala	Arg	Tyr	Arg							
	275						280								

<210> 44
 <211> 2915
 <212> DNA
 <213> Homo sapiens

<400> 44
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 ggacaggacc cgcacagcaa gcacctgtac acggccgaca tggtcacgca cgggatccag 240
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 ccgacttgga atgacctggg agacaaatac aacagcatgg aagatgccaa agtctatgtg 360
 gctaaagtgg actgcacggc ccactccgac gtgtgctccg cccagggggg gcgaggatac 420
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 ccggaagtgg aaccgcccag tgcccccgag ctcaagcaag ggctgtatga gctctcagca 600
 agcaactttg agctgcacgt tgcacaaggc gaccacttta tcaagttctt cgctccgtgg 660
 tgtggtcact gcaaagccct ggctccaacc tgggagcagc tggtctggg ccttgaacat 720
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 aaccaggttc gtggctatcc cactcttctc tggttccgag atgggaaaaa ggtggatcag 840
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<210> 45
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 45

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Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Gly	35	40	45	
Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	His	Ser	Lys	His	50	55	60	
Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	Gln	Ser	Ala	Ala	His	65	70	75	80
Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Arg	Leu	Gln	85	90	95	
Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	Tyr	Asn	Ser	Met	Glu	Asp	Ala	100	105	110	
Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	Cys	Thr	Ala	His	Ser	Asp	Val	Cys	115	120	125	
Ser	Ala	Gln	Gly	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	130	135	140	
Gly	Gln	Glu	Ala	Val	Lys	Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	145	150	155	160
Glu	Asn	Trp	Met	Leu	Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	165	170	175	
Pro	Glu	Val	Glu	Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	180	185	190	
Glu	Leu	Ser	Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	195	200	205	
Phe	Ile	Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	210	215	220	
Pro	Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	225	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	Gly	245	250	255	
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Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	Leu	Arg	Glu	275	280	285	
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Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	Glu	Pro	Glu	Ala	Asp	305	310	315	320

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 Cys Arg Thr Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu Phe
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 Pro Gly Leu Ala Gly Val Lys Ile Ala Glu Val Asp Cys Thr Ala Glu
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 Arg Asn Ile Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu
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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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<211> 762

<212> PRT

<213> Homo sapiens

<400> 48

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35 40 45

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Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala
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 Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg
 85 90 95
 Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu
 100 105 110
 Cys Ala Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile
 115 120 125
 Arg Val Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr
 130 135 140
 Phe Ala Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr
 145 150 155 160
 Leu Leu Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser
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 Pro Phe Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met
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 Leu Tyr Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu
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 Met Arg Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu
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 Arg Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 225 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe
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 Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp
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 370 375 380

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 580 585 590
 Ser His Gly Pro Ala Ala Val Pro Glu Ala Ser Ser Thr Val Tyr Asn
 595 600 605
 Gly Ser Leu Leu Leu Ile Val Gln Asp Gly Val Gly Gly Leu Tyr Gln
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 Cys Trp Ala Thr Glu Asn Gly Phe Ser Tyr Pro Val Ile Ser Tyr Trp
 625 630 635 640
 Val Asp Ser Gln Asp Gln Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly
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 Ile Pro Arg Glu His Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly
 660 665 670
 Ala Ala Leu Ala Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val
 675 680 685
 Thr Val Leu Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val
 690 695 700

Ala Ser Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys
705 710 715 720

Glu Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp Ala
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Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 49
<211> 182
<212> DNA
<213> Homo sapiens

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<223> n = g, a, c or t

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gg 182

<210> 50
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<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa = any amino acid

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Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
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 <223> n = g, a, c or t

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 gg 182

<210> 52
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 <213> Homo sapiens

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 Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
 20 25 30
 Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
 35 40 45
 Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
 50 55 60

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 <212> DNA
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 <211> 226
 <212> PRT
 <213> Homo sapiens

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 50 55 60
 Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe
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 Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly
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 Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn
 180 185 190
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 Lys Pro
 225

<210> 55
 <211> 1038
 <212> DNA
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gatgcaggag gagtataa 1038

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<210> 56
 <211> 345
 <212> PRT
 <213> Homo sapiens

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<400> 56
Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys
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Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu
      20             25             30

Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met
 35             40             45

Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu
 50             55             60

Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe
 65             70             75             80

Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
      85             90             95

Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
 100             105             110

Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
 115             120             125

Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
 130             135             140

Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
 145             150             155             160

Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
      165             170             175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
      180             185             190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
 195             200             205

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Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
 210 215 220
 Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
 225 230 235 240
 Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
 245 250 255
 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
 260 265 270
 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
 275 280 285
 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
 290 295 300
 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
 305 310 315 320
 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
 325 330 335
 Ser Pro Gln Gln Asp Ala Gly Gly Val
 340 345

<210> 57
 <211> 2457
 <212> DNA
 <213> Homo sapiens

<400> 57
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 ctgcagccct cgcctgggag agcggcgcg cgggcaggcg cccaagagag catcgagcag 180
 cggaaccgc gaagccggcc cgcagccgcg acccgcgag cctgccgctc tcccgcgcgc 240
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 tctggggatg actctgacaa cttctccggc tcaggtgcag gtgctttgca agatatcacc 420
 ttgtcacagc agacccctc cacttggaag gacacgcagc tcctgacggc tattcccacg 480
 tctccagaac ccaccggcct ggaggctaca gctgcctcca cctccaccct gccggctgga 540
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 cgggagcagg aggccacccc ccgaccagg gagaccacac agctcccag cactcatcag 660
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<210> 58

<211> 310

<212> PRT

<213> Homo sapiens

<400> 58

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Met Arg Arg Ala Ala Leu Trp Leu Trp Leu Cys Ala Leu Ala Leu Ser
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Leu Gln Pro Ala Leu Pro Gln Ile Val Ala Thr Asn Leu Pro Pro Glu
              20              25              30

Asp Gln Asp Gly Ser Gly Asp Asp Ser Asp Asn Phe Ser Gly Ser Gly
              35              40              45

Ala Gly Ala Leu Gln Asp Ile Thr Leu Ser Gln Gln Thr Pro Ser Thr
              50              55              60

Trp Lys Asp Thr Gln Leu Leu Thr Ala Ile Pro Thr Ser Pro Glu Pro
              65              70              75              80

Thr Gly Leu Glu Ala Thr Ala Ala Ser Thr Ser Thr Leu Pro Ala Gly
              85              90              95

Glu Gly Pro Lys Glu Gly Glu Ala Val Val Leu Pro Glu Val Glu Pro
              100              105              110

Gly Leu Thr Ala Arg Glu Gln Glu Ala Thr Pro Arg Pro Arg Glu Thr
              115              120              125

Thr Gln Leu Pro Thr Thr His Gln Ala Ser Thr Thr Thr Ala Thr Thr
              130              135              140

Ala Gln Glu Pro Ala Thr Ser His Pro His Arg Asp Met Gln Pro Gly
              145              150              155              160

His His Glu Thr Ser Thr Pro Ala Gly Pro Ser Gln Ala Asp Leu His
              165              170              175

Thr Pro His Thr Glu Asp Gly Gly Pro Ser Ala Thr Glu Arg Ala Ala
              180              185              190

Glu Asp Gly Ala Ser Ser Gln Leu Pro Ala Ala Glu Gly Ser Gly Glu
              195              200              205

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Gln Asp Phe Thr Phe Glu Thr Ser Gly Glu Asn Thr Ala Val Val Ala
 210 215 220
 Val Glu Pro Asp Arg Arg Asn Gln Ser Pro Val Asp Gln Gly Ala Thr
 225 230 235 240
 Gly Ala Ser Gln Gly Leu Leu Asp Arg Lys Glu Val Leu Gly Gly Val
 245 250 255
 Ile Ala Val Gly Leu Val Gly Leu Ile Phe Ala Val Cys Leu Val Gly
 260 265 270
 Phe Met Leu Tyr Arg Met Lys Lys Lys Asp Glu Gly Ser Tyr Ser Leu
 275 280 285
 Glu Glu Pro Lys Gln Ala Asn Gly Gly Ala Tyr Gln Lys Pro Thr Lys
 290 295 300
 Gln Glu Glu Phe Tyr Ala
 305 310

<210> 59
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 59
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 gtcactctga cctgcttgct gaatttctcc tgctatgggt atccgatcca attgcagtgg 180
 ctctagagg gggttccaat gaggcaggct gctgtcacct cgacctcctt gaccatcaag 240
 tctgtcttca cccggagcga gctcaagttc tccccacagt ggagtcacca tgggaagatt 300
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<210> 60
 <211> 3260
 <212> DNA
 <213> Homo sapiens

<400> 60
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<210> 61

<211> 847

<212> PRT

<213> Homo sapiens

<400> 61

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Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
  1             5             10            15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
      20             25             30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
      35             40             45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
      50             55             60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
      65             70             75             80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
      85             90             95

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Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
 100 105 110
 Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
 115 120 125
 Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
 130 135 140
 Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
 145 150 155 160
 Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
 165 170 175
 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
 180 185 190
 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
 195 200 205
 Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
 210 215 220
 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
 225 230 235 240
 Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg
 245 250 255
 Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro
 260 265 270
 Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys
 275 280 285
 Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser
 290 295 300
 Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
 305 310 315 320
 Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
 325 330 335
 Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
 340 345 350
 Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
 355 360 365
 Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
 370 375 380
 Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
 385 390 395 400
 Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
 405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
 420 425 430
 Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
 435 440 445
 Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
 450 455 460
 Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
 465 470 475 480
 Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
 485 490 495
 Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
 500 505 510
 Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
 515 520 525
 Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
 530 535 540
 Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
 545 550 555 560
 Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser
 565 570 575
 Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala
 580 585 590
 Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu
 595 600 605
 Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
 610 615 620
 Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His
 625 630 635 640
 Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
 645 650 655
 Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
 660 665 670
 Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
 675 680 685
 Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
 690 695 700
 Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
 705 710 715 720
 Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys
 725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
 740 745 750
 Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
 755 760 765
 Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
 770 775 780
 Arg Pro Pro Arg Thr Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
 785 790 795 800
 Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
 805 810 815
 Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
 820 825 830
 Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
 835 840 845

<210> 62
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 62
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 cacctacaga ccacttcaact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
 tctggtcaat gtccaggccc tcgtaggtgt gatcttcctc catgccagcc ttgctgtcat 240
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 tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 63
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 63
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 Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30
 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 64
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 64
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 gccagggagc ctgcacccag gtcacggggc gacctggctc tcaactcctg cctgggtgct 120
 cacctacaga ccacttcact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
 tctgggtcaat gtccaggccc tcgtaggtgt gatcttctc catgccagcc ttgctgtcat 240
 ccttgctccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
 tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 65
 <211> 1226
 <212> DNA
 <213> Homo sapiens

<400> 65
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 gccagatcgg aggaaccggt cccgaatccc aaaggtagtg cttgttcgcg gatctggcag 180
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<210> 66
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 66
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 20 25 30
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 35 40 45
 Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His
 50 55 60

Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln
 65 70 75 80
 Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met
 85 90 95
 Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile
 100 105 110
 Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn
 115 120 125
 Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly
 130 135 140
 Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly
 145 150 155 160
 Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro
 165 170 175
 Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu
 180 185 190
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 195 200 205
 Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu
 210 215 220
 His Pro Gly Gln Glu
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<210> 67
 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (16)
 <223> n = g, a, c or t

<400> 67
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 cctctcaagt gttgcattgt cctgcctaa accaagaagg ctaaacaag cccctcctgt 180
 ttgaattcct aaggtaagaa atttctaagc taagaaaaca ctattgccta aaaccaatga 240
 tagtggagct catttacaaa taggcattgcc tcacacacac agtccaaagg caagacactg 300
 gctttgaaat taggctcatg atgtgattcc tattatatgt acctgatttt tttaggcccc 360
 aggtatgtgg accagagtta atgtcatgac tcttcaaaga tatgatgaaa agttgcctta 420
 gaaatctaga gatgcatgtt tattaatt 449

<210> 68
 <211> 2359
 <212> DNA
 <213> Homo sapiens

<400> 68

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ttatgctaac ctctgttgct tgatgacatg tcctcaggac tctgatatta aaactcaatc 180
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gagtgaaatc tgaacgctgt cttatattaa gcagtagaat taggtattat cataaaaaagt 420
cttaatctgt agggaaatag agtttatgtt tatgagtcct gctcagtcct tctttgagag 480
aattagttga aaccagactc ctaaagctg cttttatatt tgtttgtaa gaccatttat 540
ctgcagaagg ttgcctttta accccagtggt ttctaagggtg tggaattgag tgaccctaata 600
atttacataa gagacttggt ttagtggagc ataagggagg ggcataagtt acaccgtttt 660
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<210> 69

<211> 240

<212> DNA

<213> Homo sapiens

<400> 69

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gggtccaatc attatgccaa agggctccgtc taggaggttc ttgttccaag tattgagatt 180
cccagagaaa gtaggtcccc ttagatagaa gcagagtttc tcagaggtat ttagcagcag 240
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<210> 70

<211> 980

<212> DNA

<213> Homo sapiens

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<210> 71
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 71
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 Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln
 35 40 45
 Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly
 50 55 60
 Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly
 65 70 75 80
 Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser
 85 90 95
 Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly
 100 105 110
 Pro Arg Thr Ala Glu Ala
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<210> 72
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (519)
 <223> n = g, a, c or t

<400> 72
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 tgataaaaat atttttaagc cgtgaaagtt atgagatatt ctgggtaagc ctgattatca 180
 aagaatacca caaatagctt tggagatcgt gtattgtttg tcaactgagtc aaagagatct 240
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 actccagtaa gtactcgcac aacgtacatg tgctttctcc cattgctgtc tggcttggag 360
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<210> 73
 <211> 1956
 <212> DNA
 <213> Homo sapiens

<400> 73
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 ctaactgggtc aagaataaat cccaacaagg ccaggattcc catggcagga gatacccaag 180
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 ttacaccagg tggatgctta aagtgcacaa taataattca tgttcctggg ggaagagatg 480
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 cccttcacgc cattggaaca ggaaatgccg gaaaaaaccc tatcacagtt gctgataaca 600
 taatcgatgc tattgtagac ttctcatcac aacattccac cccatcatta aaaacagtta 660
 aagttgtcat ttttcaacct gagctgctaa atatattcta cgacagcatg aaaaaagag 720
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<210> 74
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Ser Arg Ile Asn Pro Asn Lys Ala Arg Ile Pro Met Ala Gly Asp Thr
 35 40 45
 Gln Gly Val Val Gly Thr Val Ser Lys Pro Cys Phe Thr Ala Tyr Glu
 50 55 60
 Met Lys Ile Gly Ala Ile Thr Phe Gln Val Ala Thr Gly Asp Ile Ala
 65 70 75 80
 Thr Glu Gln Val Asp Val Ile Val Asn Ser Thr Ala Arg Thr Phe Asn
 85 90 95
 Arg Lys Ser Gly Val Ser Arg Ala Ile Leu Glu Gly Ala Gly Gln Ala
 100 105 110
 Val Glu Ser Glu Cys Ala Val Leu Ala Ala Gln Pro His Arg Asp Phe
 115 120 125
 Ile Ile Thr Pro Gly Gly Cys Leu Lys Cys Lys Ile Ile Ile His Val
 130 135 140
 Pro Gly Gly Lys Asp Val Arg Lys Thr Val Thr Ser Val Leu Glu Glu
 145 150 155 160
 Cys Glu Gln Arg Lys Tyr Thr Ser Val Ser Leu Pro Ala Ile Gly Thr
 165 170 175
 Gly Asn Ala Gly Lys Asn Pro Ile Thr Val Ala Asp Asn Ile Ile Asp
 180 185 190
 Ala Ile Val Asp Phe Ser Ser Gln His Ser Thr Pro Ser Leu Lys Thr
 195 200 205
 Val Lys Val Val Ile Phe Gln Pro Glu Leu Leu Asn Ile Phe Tyr Asp
 210 215 220
 Ser Met Lys Lys Arg Asp Leu Ser Ala Ser Leu Asn Phe Gln Ser Thr
 225 230 235 240
 Phe Ser Met Thr Thr Cys Asn Leu Pro Glu His Trp Thr Asp Met Asn
 245 250 255
 His Gln Leu Phe Cys Met Val Gln Leu Glu Pro Gly Gln Ser Glu Tyr
 260 265 270
 Asn Thr Ile Lys Asp Lys Phe Thr Arg Thr Cys Ser Ser Tyr Ala Ile
 275 280 285
 Glu Lys Ile Glu Arg Ile Gln Asn Ala Phe Leu Trp Gln Ser Tyr Gln
 290 295 300
 Val Lys Lys Arg Gln Met Asp Ile Lys Asn Asp His Lys Asn Asn Glu
 305 310 315 320
 Arg Leu Leu Phe His Gly Thr Asp Ala Asp Ser Val Pro Tyr Val Asn
 325 330 335

Gln His Gly Phe Asn Arg Ser Cys Ala Gly Lys Asn Ala Val Ser Tyr
 340 345 350
 Gly Lys Gly Thr Tyr Phe Ala Val Asp Ala Ser Tyr Ser Ala Lys Asp
 355 360 365
 Thr Tyr Ser Lys Pro Asp Ser Asn Gly Arg Lys His Met Tyr Val Val
 370 375 380
 Arg Val Leu Thr Gly Val Phe Thr Lys Gly Arg Ala Gly Leu Val Thr
 385 390 395 400
 Pro Pro Pro Lys Asn Pro His Asn Pro Thr Asp Leu Phe Asp Ser Val
 405 410 415
 Thr Asn Asn Thr Arg Ser Pro Lys Leu Phe Val Val Phe Phe Asp Asn
 420 425 430
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 435 440

<210> 75
 <211> 449
 <212> DNA
 <213> Homo sapiens

<400> 75
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 caggagaaca gagaaaaaac cagcctgtct ccaaactggc ccgtctcagg gactgggggc 180
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 aacagctctt ccttacagaa ggatcccaa 449

<210> 76
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 76
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 35 40 45
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 50 55 60
 His Phe Arg Glu Gly Ala Gly Leu Glu Lys Asn Gln Arg Ser Ser
 65 70 75

<210> 77
 <211> 3067
 <212> DNA
 <213> Homo sapiens

<400> 77
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 Gly Asp Thr Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg
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<211> 1364

<212> DNA

<213> Homo sapiens

<400> 94

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<210> 95

<211> 411

<212> DNA

<213> Homo sapiens

<400> 95

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<210> 96
<211> 1632
<212> DNA
<213> Homo sapiens

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<220>
<221> modified_base
<222> (1)..(1632)
<223> n = g, a, c or t

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<210> 97
<211> 2378
<212> DNA
<213> Homo sapiens

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<210> 98
<211> 313
<212> DNA
<213> Homo sapiens

<220>
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<223> n = g, a, c or t

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ataaaagtgt aaagaaatct ataccagatg tagtaacagt ggtttggttc tgggaggttg 240
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<210> 99
<211> 317
<212> DNA
<213> Homo sapiens

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<210> 100
 <211> 1968
 <212> DNA
 <213> Homo sapiens

<400> 100

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<400> 101

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 His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser
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 His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys
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 Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg
 115 120 125
 Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val
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 Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg
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 Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp
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 Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys
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 Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser
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 Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys
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 Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala
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 Lys Phe Glu Ser Met Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu Glu
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Glu Pro Glu Pro Glu Pro Glu Asn Asp Tyr Glu Asp Val Glu Glu Met
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Asp Arg His Glu Gln Glu Asp Glu Pro Glu Gly Asp Tyr Glu Glu Val
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Leu Glu Pro Glu Asp Ser Ser Phe Ser Ser Ala Leu Ala Gly Ser Ser
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Gly Cys Pro Ala Gly Ala Gly Ala Gly Ala Val Ala Leu Gly Ile Ser
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Ala Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser
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Phe Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly
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<211> 579

<212> PRT

<213> Homo sapiens

<400> 107

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Tyr Arg Gly Gln Leu Ala Ala Ser Val Leu Arg Gln Ile Ser Arg Glu
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Leu Gly Pro Gln Glu Pro Thr Gly Ser Gln Leu Leu Arg Ser Lys Lys
 65 70 75 80

Leu Pro Arg Val Arg Glu His Arg Gly Pro Leu Thr Gln Leu Arg Gly
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His Pro Pro Arg Trp Gln Pro Ile Phe Cys Val Leu Arg Gly Asp Gly
 100 105 110

Arg Leu Glu Trp Phe Ser His Lys Glu Glu Tyr Glu Asn Gly Gly His
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Cys Leu Gly Ser Thr Ala Leu Thr Gly Tyr Thr Leu Leu Thr Ser Gln
 130 135 140

Arg Glu Tyr Leu Arg Leu Leu Asp Ala Leu Cys Pro Glu Ser Leu Gly
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Asp His Thr Gln Glu Glu Pro Asp Ser Leu Leu Glu Val Pro Val Ser
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Phe Pro Leu Phe Leu Gln His Pro Phe Arg Arg His Leu Cys Phe Ser
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Ala Ala Thr Arg Glu Ala Gln His Ala Trp Arg Leu Ala Leu Gln Gly
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Gly Ile Arg Leu Gln Gly Thr Val Leu Gln Arg Ser Gln Ala Pro Ala
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Ala Arg Ala Phe Leu Asp Ala Val Arg Leu Tyr Arg Gln His Gln Gly
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His Phe Gly Asp Asp Val Thr Leu Gly Ser Asp Ala Glu Val Leu
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His Pro Leu

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<212> DNA
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<210> 109
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 109
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 Gly Ser Leu Gln Pro Leu Pro Pro Arg Phe Lys Arg Phe Phe Cys Leu
 20 25 30
 Ser Leu Gln Ser Ser Trp Asp Tyr Arg His Ala Pro Pro Arg Pro Ala
 35 40 45
 Asn Phe Val Phe Leu Val Glu Thr Gly Phe Cys His Val Ser Gln Ala
 50 55 60
 Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Pro Arg Pro Pro Lys
 65 70 75 80
 Val Leu Arg

<210> 110
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (467)
 <223> n = g, a, c or t

<400> 110
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 tgaacaaaaa agctatacat gtaggtgcat atttatctcc tcctgagttg ggagaaatct 180
 ttctaagcat agaaacaatg gtagcaaaag agaagaatag atttggctgg attaacaata 240
 aaaaatttct gccagaaata tgaaaattca atttagacaa aattcaatat aaacaaaatt 300
 aatatagaca aaggtggtta acaggtgggt ctcagagaag ataaatacat gattatttaa 360
 cataaaaaga aatgttcaat gtttctagaa gacaaataat tacaaaccta aacaaattgt 420
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 tggtaaaata tttctggaag acaatttgg 509

<210> 111
 <211> 525
 <212> DNA
 <213> Homo sapiens

<400> 111
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 caaatattgt tccccctgaa gatatgacct actagaacta ctcacatata tagtccaata 180
 attgctgact taataggtat ggtaaaatag ctgataataa gtcagactct caagagtttc 240
 tgtaccttga ttattgacaa attcattgtt ttacatccta cttaaagaaca tgtgtgtggg 300
 gaggggggtgg ggaactgggt cacaacataa tctgaaggag atcaaacatc tgtaaggaca 360
 ggtaccagat gatgataata tatctgaaaa cacaagccat ttttattctt tatcccaatt 420
 aacttgaggt actctaata tgaagcactc gattgcacta tgacctcctt gagtgatggg 480
 cagcttggtt cctctctcac ttttggtttc tttttaatat gcaaa 525

<210> 112
 <211> 183
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1)..(183)
 <223> n = g, a, c or t

<400> 112
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 ttgactttgg actgtanaag cttttctttg atcacctgtg ntggaggaaa ggaaagaagc 180
 ctt 183

<210> 113
 <211> 1750
 <212> DNA
 <213> Homo sapiens

<400> 113
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 gtggagcccc agaaccctgt gctctctgct ggagggtccc tgtttgtaga ctgcagtact 180
 gattgtccca gctctgagaa aatcgccctg gagacgtccc tatcaaagga gctgggtggcc 240
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 tgctcagtgt actgcaatgg ctcccagata acaggctcct ctaacatcac cgtgtacggg 360
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 aaaaaaaaaa 1750

<210> 114
 <211> 547
 <212> PRT
 <213> Homo sapiens

<400> 114

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Leu	Leu	Arg	Val	Glu	Pro	Gln	Asn	Pro	Val	Leu	Ser	Ala	Gly	Gly	Ser
		35					40					45			
Leu	Phe	Val	Asn	Cys	Ser	Thr	Asp	Cys	Pro	Ser	Ser	Glu	Lys	Ile	Ala
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Leu	Glu	Thr	Ser	Leu	Ser	Lys	Glu	Leu	Val	Ala	Ser	Gly	Met	Gly	Trp
65					70					75					80
Ala	Ala	Phe	Asn	Leu	Ser	Asn	Val	Thr	Gly	Asn	Ser	Arg	Ile	Leu	Cys
				85					90					95	
Ser	Val	Tyr	Cys	Asn	Gly	Ser	Gln	Ile	Thr	Gly	Ser	Ser	Asn	Ile	Thr
			100					105					110		
Val	Tyr	Gly	Leu	Pro	Glu	Arg	Val	Glu	Leu	Ala	Pro	Leu	Pro	Pro	Trp
		115					120					125			
Gln	Pro	Val	Gly	Gln	Asn	Phe	Thr	Leu	Arg	Cys	Gln	Val	Glu	Gly	Gly
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Ser	Pro	Arg	Thr	Ser	Leu	Thr	Val	Val	Leu	Leu	Arg	Trp	Glu	Glu	Glu
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Leu	Ser	Arg	Gln	Pro	Ala	Val	Glu	Glu	Pro	Ala	Glu	Val	Thr	Ala	Thr
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Val	Leu	Ala	Ser	Arg	Asp	Asp	His	Gly	Ala	Pro	Phe	Ser	Cys	Arg	Thr
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Glu	Leu	Asp	Met	Gln	Pro	Gln	Gly	Leu	Gly	Leu	Phe	Val	Asn	Thr	Ser
		195					200					205			
Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe	Val	Leu	Pro	Val	Thr	Pro	Pro	Arg
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Leu	Val	Ala	Pro	Arg	Phe	Leu	Glu	Val	Glu	Thr	Ser	Trp	Pro	Val	Asp
225					230					235					240
Cys	Thr	Leu	Asp	Gly	Leu	Phe	Pro	Ala	Ser	Glu	Ala	Gln	Val	Tyr	Leu
				245					250					255	
Ala	Leu	Gly	Asp	Gln	Met	Leu	Asn	Ala	Thr	Val	Met	Asn	His	Gly	Asp
			260					265					270		
Thr	Leu	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Arg	Ala	Asp	Gln	Glu	Gly
		275					280					285			
Ala	Arg	Glu	Ile	Val	Cys	Asn	Val	Thr	Leu	Gly	Gly	Glu	Arg	Arg	Glu
	290					295					300				
Ala	Arg	Glu	Asn	Leu	Thr	Val	Phe	Ser	Phe	Leu	Gly	Pro	Ile	Val	Asn
305					310					315					320

Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr Val Ser Cys
 325 330 335
 Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val Pro Ala Ala
 340 345 350
 Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr Glu Ser Asp
 355 360 365
 Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val Asp Gly Glu
 370 375 380
 Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu Tyr Gly Pro
 385 390 395 400
 Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp Lys Asp Lys
 405 410 415
 Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro Tyr Pro Glu
 420 425 430
 Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro Val Gly Ile
 435 440 445
 Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln Cys Gln Ala
 450 455 460
 Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met Asp Ile Glu
 465 470 475 480
 Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val Leu Leu Thr
 485 490 495
 Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val Phe Arg Glu
 500 505 510
 His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser Thr Tyr Leu
 515 520 525
 Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu Glu Pro Ser
 530 535 540
 Arg Ala Glu
 545

<210> 115
 <211> 275
 <212> DNA
 <213> Homo sapiens

<400> 115
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 tgtctattca ctctgaata tcaaataaa gagctggtag tcctgggttaa tcaacagctt 180
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<210> 116
 <211> 2040
 <212> DNA
 <213> Homo sapiens

<400> 116
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 ctacctggcg cggcgcccca agctgcagct gagcgtgtac accacgacga ggtcccacct 180
 ggggtgctgag aacaacatcg acctgggtctt gaatgtggaa gactttgatg tggagtccaa 240
 atttgaaagg acagttaatg tttctgtacc aaagaaaacg agaaacaatg ggacgctgta 300
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 cctgggtcagt cctctgacca cctacatggg ccccaagcca gaagaaatca acctgctcac 420
 cggggagtct gatacacagc agatcgaggc ggagaagaag ccgacgagtg ccctggatga 480
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<210> 117
 <211> 538
 <212> PRT
 <213> Homo sapiens

<400> 117
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 Thr Arg Pro Cys Ser Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala
 35 40 45
 Arg Arg Pro Lys Leu Gln Leu Ser Val Tyr Thr Thr Arg Ser His
 50 55 60

Leu Gly Ala Glu Asn Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe
 65 70 75 80
 Asp Val Glu Ser Lys Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys
 85 90 95
 Lys Thr Arg Asn Asn Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His
 100 105 110
 Ala Gly Val Leu Pro Trp His Asp Gly Lys Gln Val His Leu Val Ser
 115 120 125
 Pro Leu Thr Thr Tyr Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu
 130 135 140
 Thr Gly Glu Ser Asp Thr Gln Gln Ile Glu Ala Glu Lys Lys Pro Thr
 145 150 155 160
 Ser Ala Leu Asp Glu Pro Val Ser His Trp Arg Pro Arg Leu Ala Leu
 165 170 175
 Asn Val Met Ala Asp Asn Phe Val Phe Asp Gly Ser Ser Leu Pro Ala
 180 185 190
 Asp Val His Arg Tyr Met Lys Met Ile Gln Leu Gly Lys Thr Val His
 195 200 205
 Tyr Leu Pro Ile Leu Phe Ile Asp Gln Leu Ser Asn Arg Val Lys Asp
 210 215 220
 Leu Met Val Ile Asn Arg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser
 225 230 235 240
 Tyr Asp Lys Val Ser Leu Gly Arg Leu Arg Phe Trp Ile His Met Gln
 245 250 255
 Asp Ala Val Tyr Ser Leu Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala
 260 265 270
 Asp Glu Val Lys Gly Ile Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala
 275 280 285
 Leu Thr Phe Phe Val Ala Ala Phe His Leu Leu Phe Asp Phe Leu Ala
 290 295 300
 Phe Lys Asn Asp Ile Ser Phe Trp Lys Lys Lys Lys Ser Met Ile Gly
 305 310 315 320
 Met Ser Thr Lys Ala Val Leu Trp Arg Cys Phe Ser Thr Val Val Ile
 325 330 335
 Phe Leu Phe Leu Leu Asp Glu Gln Thr Ser Leu Leu Val Leu Val Pro
 340 345 350
 Ala Gly Val Gly Ala Ala Ile Glu Leu Trp Lys Val Lys Lys Ala Leu
 355 360 365
 Lys Met Thr Ile Phe Trp Arg Gly Leu Met Pro Glu Phe Gln Phe Gly
 370 375 380

Thr Tyr Ser Glu Ser Glu Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala
 385 390 395 400
 Met Lys Tyr Leu Ser Tyr Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala
 405 410 415
 Val Tyr Ser Leu Leu Asn Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu
 420 425 430
 Ile Asn Ser Phe Val Asn Gly Val Tyr Ala Phe Gly Phe Leu Phe Met
 435 440 445
 Leu Pro Gln Leu Phe Val Asn Tyr Lys Leu Lys Ser Val Ala His Leu
 450 455 460
 Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe Asn Thr Phe Ile Asp Asp
 465 470 475 480
 Val Phe Ala Phe Ile Ile Thr Met Pro Thr Ser His Arg Leu Ala Cys
 485 490 495
 Phe Arg Asp Asp Val Val Phe Leu Val Tyr Leu Tyr Gln Arg Trp Leu
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 Glu Lys Ala Thr Arg Ala Pro His Thr Asp
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<210> 118
 <211> 4217
 <212> DNA
 <213> Homo sapiens

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aagctaagac	tttttggtct	attccttttt	gcatgggtgt	ctaggggttc	tggacaatgt	3060
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aggattgtcc	agttacttta	gggggttttt	ggtgggggtt	ttccccctgt	gaaaacttac	3240
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gctggggcac	cctcaggggg	atccagagac	tcatgcccac	ggccatccat	gcgtggacgc	4020
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ggccatgtgg	ttgatttttc	taaagctgga	gaaaggaaga	attgtgcctt	gcatattact	4140
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<210> 119

<211> 923

<212> PRT

<213> Homo sapiens

<400> 119

Phe	Pro	Ala	Pro	Ala	Lys	Ala	Val	Val	Tyr	Val	Ser	Asp	Ile	Gln	Glu
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Ala Tyr Val Arg Val Leu Asp Leu His Lys Lys Pro Phe Leu Ala Lys
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 Tyr Phe Pro Phe Met Asp Leu Lys Leu Arg Ala Ala Ser Pro Ile Ile
 50 55 60
 Thr Leu Val Ala Leu Asp Glu Ala Leu Asp Asn Tyr Thr Ile Thr Phe
 65 70 75 80
 Leu Ile Arg Gly Val Ala Ile Gly Gln Thr Ser Leu Thr Ala Ser Val
 85 90 95
 Thr Asn Lys Ala Gly Gln Arg Ile Asn Ser Ala Pro Gln Gln Ile Glu
 100 105 110
 Val Phe Pro Pro Phe Arg Leu Met Pro Arg Lys Val Thr Leu Leu Ile
 115 120 125
 Gly Ala Thr Met Gln Val Thr Ser Glu Gly Gly Pro Gln Pro Gln Ser
 130 135 140
 Asn Ile Leu Phe Ser Ile Ser Asn Glu Ser Val Ala Leu Val Ser Ala
 145 150 155 160
 Ala Gly Leu Val Gln Gly Leu Ala Ile Gly Asn Gly Thr Val Ser Gly
 165 170 175
 Leu Val Gln Ala Val Asp Ala Glu Thr Gly Lys Val Val Ile Ile Ser
 180 185 190
 Gln Asp Leu Val Gln Val Glu Val Leu Leu Leu Arg Ala Val Arg Ile
 195 200 205
 Arg Ala Pro Ile Met Arg Met Arg Thr Gly Thr Gln Met Pro Ile Tyr
 210 215 220
 Val Thr Gly Ile Thr Asn His Gln Asn Pro Phe Ser Phe Gly Asn Ala
 225 230 235 240
 Val Pro Gly Leu Thr Phe His Trp Ser Val Thr Lys Arg Asp Val Leu
 245 250 255
 Asp Leu Arg Gly Arg His His Glu Ala Ser Ile Arg Leu Pro Ser Gln
 260 265 270
 Tyr Asn Phe Ala Met Asn Val Leu Gly Arg Val Lys Gly Arg Thr Gly
 275 280 285
 Leu Arg Val Val Val Lys Ala Val Asp Pro Thr Ser Gly Gln Leu Tyr
 290 295 300
 Gly Leu Ala Arg Glu Leu Ser Asp Glu Ile Gln Val Gln Val Phe Glu
 305 310 315 320
 Lys Leu Gln Leu Leu Asn Pro Glu Ile Glu Ala Glu Gln Ile Leu Met
 325 330 335
 Ser Pro Asn Ser Tyr Ile Lys Leu Gln Thr Asn Arg Asp Gly Ala Ala
 340 345 350

Ser Leu Ser Tyr Arg Val Leu Asp Gly Pro Glu Lys Val Pro Val Val
 355 360 365
 His Val Asp Glu Lys Gly Phe Leu Ala Ser Gly Ser Met Ile Gly Thr
 370 375 380
 Ser Thr Ile Glu Val Ile Ala Gln Glu Pro Phe Gly Ala Asn Gln Thr
 385 390 395 400
 Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser
 405 410 415
 Met Ser Pro Val Leu His Thr Gln Asn Lys Glu Ala Leu Val Ala Val
 420 425 430
 Pro Leu Gly Met Thr Val Thr Phe Thr Val His Phe His Asp Asn Ser
 435 440 445
 Gly Asp Val Phe His Ala His Ser Ser Val Leu Asn Phe Ala Thr Asn
 450 455 460
 Arg Asp Asp Phe Val Gln Ile Gly Lys Gly Pro Thr Asn Asn Thr Cys
 465 470 475 480
 Val Val Arg Thr Val Ser Val Gly Leu Thr Leu Leu Arg Val Trp Asp
 485 490 495
 Ala Glu His Pro Gly Leu Ser Asp Phe Met Pro Leu Pro Val Leu Gln
 500 505 510
 Ala Ile Ser Pro Glu Leu Ser Gly Ala Met Val Val Gly Asp Val Leu
 515 520 525
 Cys Leu Ala Thr Val Leu Thr Ser Leu Glu Gly Leu Ser Gly Thr Trp
 530 535 540
 Ser Ser Ser Ala Asn Ser Ile Leu His Ile Asp Pro Lys Thr Gly Val
 545 550 555 560
 Ala Val Ala Arg Ala Val Gly Ser Val Thr Val Tyr Tyr Glu Val Ala
 565 570 575
 Gly His Leu Arg Thr Tyr Lys Glu Val Val Val Ser Val Pro Gln Arg
 580 585 590
 Ile Met Ala Arg His Leu His Pro Ile Gln Thr Ser Phe Gln Glu Ala
 595 600 605
 Thr Ala Ser Lys Val Ile Val Ala Val Gly Asp Arg Ser Ser Asn Leu
 610 615 620
 Arg Gly Glu Cys Thr Pro Thr Gln Arg Glu Val Ile Gln Ala Leu His
 625 630 635 640
 Pro Glu Thr Leu Ile Ser Cys Gln Ser Gln Phe Lys Pro Ala Val Phe
 645 650 655
 Asp Phe Pro Ser Gln Asp Val Phe Thr Val Glu Pro Gln Phe Asp Thr
 660 665 670

Ala Leu Gly Gln Tyr Phe Cys Ser Ile Thr Met His Arg Leu Thr Asp
 675 680 685
 Lys Gln Arg Lys His Leu Ser Met Lys Lys Thr Ala Leu Val Val Ser
 690 695 700
 Ala Ser Leu Ser Ser Ser His Phe Ser Thr Glu Gln Val Gly Ala Glu
 705 710 715 720
 Val Pro Phe Ser Pro Gly Leu Phe Ala Asp Gln Ala Glu Ile Leu Leu
 725 730 735
 Ser Asn His Tyr Thr Ser Ser Glu Ile Arg Val Phe Gly Ala Pro Glu
 740 745 750
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 755 760 765
 Phe Ala Lys Glu Lys Ser Phe Gly Trp Pro Ser Phe Ile Thr Tyr Thr
 770 775 780
 Val Gly Val Ser Asp Pro Ala Ala Gly Ser Gln Gly Pro Leu Ser Thr
 785 790 795 800
 Thr Leu Thr Phe Ser Ser Pro Val Thr Asn Gln Ala Ile Ala Ile Pro
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 Ala Ser Leu Phe Gln His Phe Leu Asp Ser Tyr Gln Val Met Phe Phe
 835 840 845
 Thr Leu Phe Ala Leu Leu Ala Gly Thr Ala Val Met Ile Ile Ala Tyr
 850 855 860
 His Thr Val Cys Thr Pro Arg Asp Leu Ala Val Pro Ala Ala Leu Thr
 865 870 875 880
 Pro Arg Ala Ser Pro Gly His Ser Pro His Tyr Phe Ala Ala Ser Ser
 885 890 895
 Pro Thr Ser Pro Asn Ala Leu Pro Pro Ala Arg Lys Ala Ser Pro Pro
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 Ser Gly Leu Trp Ser Pro Ala Tyr Ala Ser His
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<210> 120
 <211> 1270
 <212> PRT
 <213> Homo sapiens

<400> 120
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 35 40 45
 Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser Gly Met Phe Ser
 50 55 60
 Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu His Ile Met Val
 65 70 75 80
 Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val Leu Ser Thr Leu
 85 90 95
 Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu Ser Lys Pro Gln
 100 105 110
 Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile Leu Gly Phe Leu
 115 120 125
 Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn Ser Asn Ile Ser
 130 135 140
 Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu Asn Glu Arg Ser
 145 150 155 160
 Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg Met Ser Thr Tyr
 165 170 175
 His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys Glu Lys Arg Glu
 180 185 190
 Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile Gln Lys Thr Val
 195 200 205
 Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln Gln Thr Leu Glu
 210 215 220
 Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly Glu Arg Glu Val
 225 230 235 240
 Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr Met Leu Lys Ala
 245 250 255
 Trp Gln His Tyr Leu Ala Ser Glu Lys Lys Ser Leu Ala Ser Arg Ser
 260 265 270
 Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser Gly Ser Leu Ser
 275 280 285
 Ser Ala Met Lys Leu Met Pro Gly Arg Gln Ala Lys Asp Pro Glu Cys
 290 295 300
 Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr Arg Arg Arg Gly
 305 310 315 320
 Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val Gln Arg Arg Lys
 325 330 335
 Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg Ile Gln Glu Gln
 340 345 350

Leu Phe Gly Glu Leu Gly Leu Trp Ser Gln Gly Glu Glu Thr Lys Pro
 355 360 365
 Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro Ala Arg Met Arg
 370 375 380
 Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu Ser Ser Gly Arg
 385 390 395 400
 His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser Gln Thr Asn Ala
 405 410 415
 Glu Asn Gln Asp Glu Leu Thr Leu Arg Glu Ala Glu Gly Glu Pro Asp
 420 425 430
 Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe Pro Ala Leu His
 435 440 445
 Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys Arg Glu Arg Gln
 450 455 460
 Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val Thr Gln Lys Phe
 465 470 475 480
 Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu Gly Val Leu Leu
 485 490 495
 Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe Thr Leu Ser Pro
 500 505 510
 Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser Asn Ile Ser Asp
 515 520 525
 Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser Thr Asp His Tyr
 530 535 540
 Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu Leu Arg Gln Ala
 545 550 555 560
 Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe Phe His Asn Gly
 565 570 575
 Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg Ser Lys Ala Phe
 580 585 590
 Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser
 595 600 605
 Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met
 610 615 620
 Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met
 625 630 635 640
 Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr
 645 650 655
 Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn
 660 665 670

Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala
 675 680 685
 Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val
 690 695 700
 Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr His
 705 710 715 720
 Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro
 725 730 735
 Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val Ala
 740 745 750
 Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser Arg
 755 760 765
 Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr Leu
 770 775 780
 Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met Gln
 785 790 795 800
 Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp Gly
 805 810 815
 Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp
 820 825 830
 Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly Tyr
 835 840 845
 Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro
 850 855 860
 Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro Leu
 865 870 875 880
 Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val Pro
 885 890 895
 Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly Lys
 900 905 910
 Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly His
 915 920 925
 Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln Val
 930 935 940
 Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro Lys
 945 950 955 960
 Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala Val
 965 970 975
 Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe Ser
 980 985 990

Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser Asp
 995 1000 1005
 Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu
 1010 1015 1020
 Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser
 1025 1030 1035 1040
 Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg
 1045 1050 1055
 Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr
 1060 1065 1070
 Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln
 1075 1080 1085
 Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr
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 Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp
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 Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp
 1125 1130 1135
 Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro
 1140 1145 1150
 Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp
 1155 1160 1165
 Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val
 1170 1175 1180
 Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly
 1185 1190 1195 1200
 Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu
 1205 1210 1215
 Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr
 1220 1225 1230
 Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser
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 Cys Trp Ser Ala Asp Gly
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<210> 121

<211> 647

<212> PRT

<213> Homo sapiens

<400> 121
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 35 40 45
 Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly
 50 55 60
 Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu
 65 70 75 80
 Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr
 85 90 95
 His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro
 100 105 110
 Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val
 115 120 125
 Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser
 130 135 140
 Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr
 145 150 155 160
 Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met
 165 170 175
 Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp
 180 185 190
 Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser
 195 200 205
 Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly
 210 215 220
 Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His
 225 230 235 240
 Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro
 245 250 255
 Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val
 260 265 270
 Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly
 275 280 285
 Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly
 290 295 300
 His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln
 305 310 315 320

Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro
 325 330 335
 Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala
 340 345 350
 Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe
 355 360 365
 Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser
 370 375 380
 Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys
 385 390 395 400
 Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr
 405 410 415
 Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro
 420 425 430
 Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val
 435 440 445
 Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser
 450 455 460
 Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val
 465 470 475 480
 Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser
 485 490 495
 Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu
 500 505 510
 Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly
 515 520 525
 Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp
 530 535 540
 Asp Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg
 545 550 555 560
 Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala
 565 570 575
 Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp
 580 585 590
 Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu
 595 600 605
 Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val
 610 615 620

Ser Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile
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Phe Cys Trp Ser Ala Asp Gly
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<213> Artificial Sequence

<220>
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amplification primer PDM-797

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<210> 123
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer PDM-799

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<210> 124
<211> 980
<212> DNA
<213> Homo sapiens

<400> 124
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tgctttctatc taaggggacc tactttctctc gggaatctca atacttggaa caagaacctc 180
ctagacggac cctttggcat aatgaattgg accaactgta ggttccagga ctagagagcc 240
agcaatgcct ccatgaacaa tctcacccaa ttactctgct caggaaacga ggtaactgat 300
ggacagccga ggcagccct taggcggctt aggcctcccc tgtggagcat ccctgaggcg 360
gactccggcc agcccgagt atgcgatcca aagagcactc ccgggtagga aattgccccg 420
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gaacaccggg aagggaactg cacttgaggc ccggacatct gaaacttgta gactgggagc 540
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gccctgctcc agtcacaccc ggaagctgac tgggtccacgc acagctgaag catgaggaaa 660
ctcatcgcg gactaatatt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720
cttcctcaga ctgagaactg tttccagtat atacatcaag tcaactgagg aggacaaaag 780
attgctacat tcctattatt ttaagggttac atttttgggg acccctcttt cttctgttct 840
agctattacc tttcttgtgt cacctagaaa aggaccagtc ctttaattgta ttttaaaaac 900
tgtgatcatg ggaagcttta aattgggttca ataacacgca tcaagttggg tatttcctgg 960
gctacatacc ttggatagat 980

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